

09/990832

GenCore version 5.1.6
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ON protein - protein search, using sw model

Run on: October 2, 2003, 11:46:19 : Search time 41 seconds
Database: 11/07/03
27,130 Million cells, updates/week

Title: US-09-990 832c-51
Perfect score: 35
Sequence: 1: SIQVPLP 7

Scoring table: BLASTSUM2

Gapop 10.0, Gapext 0.5

Searched: 1107961 seqs, 15970573 results

Total number of hits satisfying chosen parameters: 110766

Minimum DB seq length: 0

Maximum DB seq length: 230306000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneset_29Feb03

1:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
2:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
3:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
4:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
5:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
6:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
7:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
8:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
9:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
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11:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
12:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
13:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
14:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
15:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
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17:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
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19:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
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21:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
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23:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35
24:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT	35

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	38	97.4	57	23	AMPOC11
2	35	95.7	325	21	AM11587
3	35	95.7	754	22	AM64352
4	34	87.2	164	22	AM65577
5	34	87.2	164	22	AM64017
6	34	87.2	164	22	AM64017
7	34	87.2	164	22	AM64017
8	34	87.2	164	22	AM64017
9	34	87.2	164	22	AM64017

1	34	87.2	164	22	AM14102
2	34	87.2	164	22	AM14102
3	34	87.2	164	22	AM14102
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5	34	87.2	164	22	AM14102
6	34	87.2	164	22	AM14102
7	34	87.2	164	22	AM14102
8	34	87.2	164	22	AM14102
9	34	87.2	164	22	AM14102
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11	34	87.2	164	22	AM14102
12	34	87.2	164	22	AM14102
13	34	87.2	164	22	AM14102
14	34	87.2	164	22	AM14102
15	34	87.2	164	22	AM14102
16	34	87.2	164	22	AM14102
17	34	87.2	164	22	AM14102
18	34	87.2	164	22	AM14102
19	34	87.2	164	22	AM14102
20	34	87.2	164	22	AM14102
21	34	87.2	164	22	AM14102
22	34	87.2	164	22	AM14102
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25	34	87.2	164	22	AM14102
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35	34	87.2	164	22	AM14102
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38	34	87.2	164	22	AM14102
39	34	87.2	164	22	AM14102
40	34	87.2	164	22	AM14102
41	34	87.2	164	22	AM14102
42	34	87.2	164	22	AM14102
43	34	87.2	164	22	AM14102
44	34	87.2	164	22	AM14102
45	34	87.2	164	22	AM14102

AL:30NM:MTS

PEPIDE 1

XX App0011 standard: Protein: 57 AA.

XX App0011:

XX 24-JUN-2002 (first entry)

XX Human GRFX protein sequence SEQ ID NO:16004

XX Human, upper respiratory tract, cancer, cirrhosis, hyperproliferative disorder, psoriasis, benign tumor, haemorrhage, degenerative disorder, osteoarthritis, neurodegenerative disorder, cardiovascular disease, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, immune deficiency, immune disorder, infectious disease, autoimmune disorder, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis.

XX Human, sapiens.

XX W2C0119253-A2

XX C6-DEG-2001

XX 29-MAY-2001: ZC01W0-010876.

XX 31-MAY-2001: ZC01W0-010876.

XX 29-MAY-2001: ZC01W0-010876.

XX (C6-DEG-2001) CORRECTION.

ID ABB24716 standard; Protein; 164 AA.
 AC ABB24716;
 XX
 XX 23-JAN-2002 (first entry)
 XX
 XX Protein: 6715 encoded by probe for measuring heart cell gene expression
 XX
 XX Human: gene expression: heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease
 XX
 XX Homo sapiens.
 OS
 PN W0200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001: 2001WO-US00646.
 XX
 XX 04-FEB-2000: 2000US-C180312.
 PR 26-MAY-2000: 2000US-C207456.
 PR 30-JUN-2000: 2000US-C608468.
 PR 03-AUG-2000: 2000US-C632366.
 PR 21-SEP-2000: 2000US-C234687.
 PR 27-SEP-2000: 2000US-C236359.
 PR 04-OCT-2000: 2000US-C24263.
 XX
 XX (NOTE: MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR.
 PI WPI: 2001-481446/53.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX
 XX Claim 15: SEQ ID NO 6456: 530pp: English.
 XX
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays
 CC by measuring gene expression, the probes are useful for predicting,
 CC diagnosis, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system, i.e. cardiovascular disease.
 CC Human heart gene expression is measured using the probes.
 CC Note: The sequence data for this patent did not form part of the claimed
 CC specification, but was obtained in electronic format directly from WPI.
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 164 AA:
 Query Match B7.24; Score 41; OF 22; Length 164;
 Best Local Similarity 71.4%; Pred. No. 1.2e-02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
 UY : SIGVPLP 7
 Db 92 ALVPLP 95
 RESULT 7
 ID AAM61116 standard; Protein; 164 AA.
 AC AAM61116;
 XX
 XX 05-NOV-2001 (first entry)
 XX
 XX Human brain expressed single exon probe encoded protein SEQ ID NO: 34131.

KW Human brain expressed exon, gene expression analysis: probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer
 XX
 XX Homo sapiens.
 OS
 PN W0200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001: 2001WO-US00646.
 XX
 XX 04-FEB-2000: 2000US-C180312.
 PR 26-MAY-2000: 2000US-C207456.
 PR 30-JUN-2000: 2000US-C608468.
 PR 03-AUG-2000: 2000US-C632366.
 PR 21-SEP-2000: 2000US-C234687.
 PR 27-SEP-2000: 2000US-C236359.
 PR 04-OCT-2000: 2000US-C24263.
 XX
 XX (NOTE: MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR.
 PI WPI: 2001-481446/53.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX
 XX Claim 15: SEQ ID NO: 34223: 650pp: Sequence listing: English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancer. The present sequence is a protein encoded by one of
 CC the probes of the invention.
 XX
 XX Sequence 164 AA:
 Query Match B7.24; Score 41; OF 22; Length 164;
 Best Local Similarity 71.4%; Pred. No. 1.2e-02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
 UY : SIGVPLP 7
 Db 92 ALVPLP 98
 RESULT 8
 ID AAM31927 standard; Protein; 114 AA.
 AC AAM31927;
 XX
 XX 09-NOV-2001 (first entry)
 XX
 XX Human brain marrow expressed probe encoded protein SEQ ID NO: 34131.
 KW microarray; cancer; leukemia; lymphoma; myeloma.
 XX
 XX Homo sapiens
 OS
 PN W0200157274-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001: 2001WO-US00646.
 PR 24-FEB-2000: 2000US-C180312.
 PR 26-MAY-2000: 2000US-C207456.

PR 30-JUN-2003: 2000US-0604163.
 PR 01-AUG-2003: 2000US-0612466.
 PR 21-SEP-2003: 2000US-0234567.
 PR 27-SEP-2003: 2000US-0436159.
 PR 04-OCT-2003: 2000US-0024241.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn ST, Hanzel DK, Chen W, Rank DR:
 XX WPI, 2001-488401/53.
 XX Human genome-derived single exon nuclear acid probes useful for
 XX analyzing gene expression in human bone marrow.
 XX Example 4: SEQ ID NO: 34131; 654pp + Sequence Listing, English.
 XX The present invention provides a number of single exon nuclear acid
 XX probes which are derived from genomic sequences expressed in the human
 XX bone marrow. They can be used to measure gene expression in human marrow
 XX samples which may enable the improved diagnosis and treatment of cancers
 XX and lymphomas. The present invention provides a sequence listing of a
 XX protein encoded by one of the probes of the invention.
 XX Sequence 164 AA:
 SQ
 Query Match: 87.24; Score 34; DB 22; Length 164;
 Best Local Similarity: 71.44; Pred. No. 1,2c-02;
 Matches: 5; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;
 QY 1 SIGYPLP 7
 DB 92 ADGYPLP 98
 RESULT 9
 ID AM20115 standard; Protein: 164 AA.
 XX AM20115:
 XX 12-OCT-2001 (first entry)
 XX Peptide 16549 encoded by probe for measuring cervical gene expression.
 XX Probe: human; microarray: gene expression; cervical; epithelial cell.
 XX cervical cancer
 XX Humo sapiens.
 XX W200157270-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001: 2001US-0805570.
 XX 04-FEB-2003: 2000US-0283112.
 XX 26-MAY-2003: 2000US-0204256.
 XX 01-JUN-2003: 2000US-0604006.
 XX 21-SEP-2003: 2000US-0234567.
 XX 27-SEP-2003: 2000US-0234567.
 XX 04-OCT-2003: 2000US-0244163.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn ST, Hanzel DK, Chen W, Rank DR:
 XX WPI, 2001-488401/53.
 XX Human genome-derived single exon nuclear acid probes useful for
 XX analyzing gene expression in human cervical epithelial cells.

US Data 27: SEQ ID NO: 34131; 454pp; English.
 XX The present invention relates to human single exon nuclear acid probes
 XX (SEQ. See AA15546-AA15549). The present sequence is a peptide encoded
 XX by one such probe. The SEQs are derived from human B26 cells. The SEQs
 XX can be used to produce a single exon microarray, which can be used for
 XX measuring human gene expression in a sample derived from human cervical
 XX epithelial cells. By measuring gene expression, the probes are therefore
 XX useful in grading and/or staging of diseases of the cervix, notably
 XX cervical cancer.
 XX Sequence data for this patent did not form part of the printed
 XX sequence, but was deposited with the National Center for Human Genome
 XX Research, and is available from the National Center for Human Genome
 XX Research, 4015 Reservoir Road, Bethesda, MD 20814-4505, USA.
 XX Sequence 154 AA:
 SQ
 Query Match: 87.24; Score 34; DB 22; Length 164;
 Best Local Similarity: 71.44; Pred. No. 1,2c-02;
 Matches: 5; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;
 QY 1 SIGYPLP 7
 DB 92 ADGYPLP 98
 RESULT 10
 ID AM20115 standard; Protein: 164 AA.
 XX AM20115:
 XX 12-OCT-2001 (first entry)
 XX Peptide 16549 encoded by probe for measuring placental gene expression.
 XX Probe: human; placenta; antenatal diagnosis;
 XX genetic disorder.
 XX Humo sapiens.
 XX W200157270-A2.
 XX 09-AUG-2001
 XX 30-JAN-2001: 2001US-0805570.
 XX 04-FEB-2003: 2000US-0180322.
 XX 26-MAY-2003: 2000US-0204256.
 XX 01-JUN-2003: 2000US-0604006.
 XX 21-SEP-2003: 2000US-0234567.
 XX 27-SEP-2003: 2000US-0234567.
 XX 04-OCT-2003: 2000US-0244163.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn ST, Hanzel DK, Chen W, Rank DR:
 XX WPI, 2001-488401/53.
 XX Human genome-derived single exon nuclear acid probes useful for
 XX analyzing gene expression in human placenta.
 XX Data 27: SEQ ID NO: 34131; 654pp; English
 XX The present invention relates to single exon nuclear acid probes (SEQ.
 XX See AA15546-AA15549). The present sequence is a peptide encoded by one
 XX such probe. The probes are useful for producing a microarray for
 XX predicting, measuring and displaying gene expression in samples derived
 XX from human placenta. The probes are useful for antenatal diagnosis of
 XX human genetic disorders.
 XX Sequence 164 AA:
 SQ

PT Cytokine-like factor 1 (CLF-1) and interleukin (IL)-6/60 complex.
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for
 PT treating inflammatory and autoimmune disorders.

XX Claim 1: Page 15-16: 67pp. English.

XX The present sequence is that of human interleukin-B60 (IL-60), a
 CC novel, small, soluble cytokine-like protein that exhibits structural
 CC motifs characteristic of a member of the long-chain cytokines and
 CC which shows homology to granulocyte colony stimulating factor and
 CC interleukin-6. IL-60 may have either stimulatory or inhibitory
 CC effects on haematopoietic cells, including e.g. lymphoid cells,
 CC such as T-cells, B-cells, natural killer cells, macrophages,
 CC dendritic cells, haematopoietic progenitors, etc. Methods are
 CC provided for modulating the physiology or development of a cell or
 CC tissue culture cells by contacting the cell with an agonist or
 CC antagonist of IL-60 or an antagonist of a complex of
 CC antagonist IL-60 and its partner, cytokine-like factor-1 (CLF-1).
 CC AAB19587: The IL-60/CLF-1 cytokine serves as a key physiological
 CC factor in motor neuron development and regeneration. IL-60, its
 CC agonists and antagonists may be used to treat inflammatory or
 CC autoimmune disorders and also for drug screening.

XX Sequence 215 AA:

Query Match 87.2% Score 34: DB 21: Length 215;
 Best Local Similarity 71.4% Pred. No. 1.5e-02;
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

QY 1 SWYSP 7
 11111
 DB 143 ALQYSP 149

RESULT 13

AAB19587 standard: Protein: 215 AA.

XX AAB19587:

XX 22-JAN-2001 (first entry)

XX Mouse interleukin-B60 (IL-60).

XX Interleukin-B60; IL-60; mouse; cytokine; cytokine-like factor-1;
 XX haematopoietic; inflammation; anti-inflammatory; autoimmune disease;
 XX therapy.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1-17

XX Protein /Label: Signal_peptide

XX 18-215 /Label: Mature-protein

XX W020007631-A1.

XX 14-SEP-2000.

XX 09-MAR-2000: 2000NC-0505:82.

XX 11-MAR-1999: 99US-0267401.

XX (SCHE) SCHERING CORP.

XX Oppmann B, Timans JC, Kastelen RA, Bazan JF:

XX WPI: 2003-567425/55

XX N-PS08: AAB19547.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-6/60 complex
 XX polypeptides, and nucleic acids, useful in research, diagnosis and for

PT treating inflammatory and autoimmune disorders.
 XX Claim 1: Page 17: 67pp. English.

XX The present sequence is that of mouse interleukin B60 (IL-B60), a
 CC novel, small, soluble cytokine-like protein that exhibits structural
 CC motifs characteristic of a member of the long-chain cytokines and
 CC which shows homology to granulocyte colony stimulating factor and
 CC interleukin-6. IL-60 may have either stimulatory or inhibitory
 CC effects on haematopoietic cells, including e.g. lymphoid cells,
 CC such as T-cells, B-cells, natural killer cells, macrophages,
 CC dendritic cells, haematopoietic progenitors, etc. Methods are
 CC provided for modulating the physiology or development of a cell or
 CC tissue culture cells by contacting the cell with an agonist or
 CC antagonist of IL-B60 or an antagonist of a complex of
 CC antagonist IL-B60 and its partner, cytokine-like factor-1 (CLF-1).
 CC AAB19587: The IL-60/CLF-1 cytokine serves as a key physiological
 CC factor in motor neuron development and regeneration. IL-60, its
 CC agonists and antagonists may be used to treat inflammatory or
 CC autoimmune disorders and also for drug screening.

XX Sequence 215 AA:

Query Match 87.2% Score 34: DB 21: Length 215;
 Best Local Similarity 71.4% Pred. No. 1.5e-02;
 Matches 5: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

QY 1 SWYSP 7
 11111
 DB 143 ALQYSP 149

RESULT 14

AAB19587 standard: Protein: 215 AA.

XX AAB19587:

XX 02-JUL-2001 (first entry)

XX Human cardiotrophin-like cytokine (CLC) protein.

XX Human, biologically active complex: haemopoietin receptor; N86;

XX cardiotrophin like cytokine; CLC; therapy; prophylaxis; proliferation;

XX differentiation; cell survival; neurotrophic activity.

XX Homo sapiens

XX Key Location/Qualifiers

XX Peptide 1-17

XX Protein /Label: Signal_peptide

XX 18-215 /Label: Mature-protein

XX W0200127157-A1

XX 19-SEP-2000.

XX 06-SEP-2000: 2000NC-0461116.

XX 06-SEP-1999: 99AU-0303723.

XX 12-MAY-2000: 2000AU-0307463.

XX (ANSA) ANSA OPERATIONS VCY LTD.

XX N86; A. K. Gupta RM, Puri LJ, Reid K, Bartlett PE, Hilton DJ.

XX N86; A. K. Gupta RM, Puri LJ, Reid K, Bartlett PE, Hilton DJ.

XX WPI: 2003-567425/55

XX N-PS08: AAB19547.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-6/60 complex
 XX polypeptides, and nucleic acids, useful in research, diagnosis and for

PT cardiostrophin-like cytokine, for facilitating proliferation,
PT differentiation and/or survival of a cell -
XX Claim 32: Para 114-115: 12pp: English.
XX The present invention relates to a biologically active complex comprising
CC a hemopoietin receptor, 886 and cardiostrophin-like cytokine (CLC).
CC The complex is useful in the manufacture of a medicament for the
CC treatment and/or prophylaxis of a subject, as it is involved in
CC facilitating proliferation, differentiation and/or survival of a cell.
CC The complex or its components have neurotrophic activity. The present
CC sequence is human cardiostrophin-like cytokine (CLC) protein.
XX Sequence 223 AA:
Query Match: 47.2%, Score 34, 25 223 Length 223
Best Local Similarity: 71.4%, Pred. No. 1.6e+02,
Matches 5: Conservative 2: Mismatches 6: Indels 0: Gaps 0:
Qy 1 SIGYPLP 7
Db 153 AIGYPLP 159
RESULT 15
AAW29715
AAW29715 Standard: Protein: 225 AA.
AC AAW29715:
XX 30-NOV-1998 (first entry)
XX Human neurotrophic factor NNT-1.
XX NNT-1: neurotrophic factor; human; anti-inflammatory; adjuvant.
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth Syndrome;
KW cerebellar ataxia; Charcot-Marie-Tooth Syndrome;
KW common variable immunodeficiency; HIV infection; HIV infection;
KW hypogammaglobulinemia; X-linked agammaglobulinemia; antisepsis;
KW therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..27
FI /Label= Sig_pept.db
FI 28..225
FI /Label= Mat_protein
XX WC9813922-A1
XX 05-AUG-1998.
XX 02-FEB-1996: 98W0-US92163.
XX 30-JAN-1998: 98US-001634.
XX 03-FEB-1997: 97US-0792015.
XX (AMGE-) AMGEN INC.
XX Chong W, Elliot GS, Sarantis H, Senaldi G,
XX NFI: 1998-437475/37.
XX N-PSDB: AAW47510, AAW47511.
XX Newly isolated nucleic acid encoding human or murine neurotrophic
XX factor NNT-1 - useful for treatment of neurological, and
XX immunological diseases or inflammation, also as vaccine adjuvant.
XX Claim 12: Fig 1, 12pp: English.
XX This is the amino acid sequence of a novel neurotrophic factor.

CC designated NNT-1, that is a growth factor for neurons and for H or
CC cells. It was deduced from isolated cDNA (see AAW47510) and
CC genomic DNA (see AAW47511) clones. Vectors containing the cDNA or
CC genomic DNA were used to produce recombinant proteins. The
CC of NNT-1 polypeptides. These are used to treat: (i) neurological
CC or immunological diseases, specifically Alzheimer's, Parkinson's
CC or Huntington's disease, amyotrophic lateral sclerosis,
CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
CC degeneration of the neural retina, or conditions characterised by
CC or B cell defects, e.g. common variable immunodeficiency (CVID),
CC selective IgA deficiency, hypogammaglobulinemia and X-linked
CC agammaglobulinemia (claimed), but many others disclosed; and (ii)
CC inflammation. NNT-1 is also able to boost immunoreactivity and
CC antibody production following vaccination, and, since it inhibits
CC tumour growth, it may be used in the treatment of cancer. NNT-1
CC may be used as a vaccine adjuvant. Cells that have been engineered to
XX express NNT-1 can be implanted, or nucleic acids are delivered in
XX gene therapy vectors
XX Sequence 225 AA:
Query Match: 47.2%, Score 14, 14 16 Length 225.
Best Local Similarity: 71.4%, Pred. No. 1.6e+02,
Matches 5: Conservative 2: Mismatches 6: Indels 0: Gaps 0:
Qy 1 SIGYPLP 7
Db 153 AIGYPLP 159
Stat: 0.0, computed: 0.000000, 2.2600, 13.5500
Clp time: 1.43 secs


```

1 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
2
3 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
4
5 FILE REFERENCE: APOC100001
6
7 CURRENT APPLICATION NUMBER: US/09/864,761
8
9 PRIOR FILING DATE: 2001-05-23
10
11 PRIOR APPLICATION NUMBER: US 62/180,312
12
13 PRIOR FILING DATE: 2000-02-04
14
15 PRIOR APPLICATION NUMBER: US 60/207,455
16
17 PRIOR FILING DATE: 2000-05-26
18
19 PRIOR APPLICATION NUMBER: US 09/632,366
20
21 PRIOR FILING DATE: 2000-08-03
22
23 PRIOR APPLICATION NUMBER: US 60/242,636
24
25 PRIOR FILING DATE: 2000-10-04
26
27 PRIOR APPLICATION NUMBER: US 60/236,355
28
29 PRIOR FILING DATE: 2000-09-27
30
31 PRIOR APPLICATION NUMBER: PCT/US01/006666
32
33 PRIOR FILING DATE: 2001-01-10
34
35 PRIOR APPLICATION NUMBER: PCT/US01/006667
36
37 PRIOR FILING DATE: 2001-01-10
38
39 PRIOR APPLICATION NUMBER: PCT/US01/006668
40
41 PRIOR APPLICATION NUMBER: PCT/US01/006669
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65 PRIOR APPLICATION NUMBER: US 60/234,698
66
67 PRIOR FILING DATE: 2000-09-21
68
69 PRIOR APPLICATION NUMBER: US 60/234,699
70
71 PRIOR FILING DATE: 2001-01-20
72
73 NUMBER OF SEQ ID NOS: 49117
74
75 SOFTWARE: Annonax Sequence Listing Engine ver. 1.1
76
77 SEQ ID NO 40014
78
79 LENGTH: 154
80
81 TYPE: PRT
82
83 ORGANISM: Homo sapiens
84
85 FEATURE:
86
87 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4, 2
88
89 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4, 1
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91 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4, 1
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93 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4, 1
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95 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4, 4
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97 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4, 2
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99 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4, 4
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101 OTHER INFORMATION: EXPRESSED IN FRIL LIVER, SIGNAL = 4, 5
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103 OTHER INFORMATION: EXPRESSED IN HEPG2, SIGNAL = 4, 5
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105 OTHER INFORMATION: SWISSPROT HIT: A03056, EVALUE 6.00e-01
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Query Match	87.28	Score 34	28 9	Length 164
Best Local Similarity	71.48	Prod. No. 84		
Matches 5	Conservative	2	Mismatches 0	Indels 0
Gaps				

Qy 1 SIGYPLP 7
DB 92 AIGYPLP 96

RESULT 3
US-09-931-704-2

US-09-931-704-2
: Sequence 2, Application US/09931704

```

: Patent No. US20020041873A1
:
: GENERAL INFORMATION:
:   TITLE OF INVENTION:  Glycerol
:   FIELD OF INVENTION:  Methods and Compositions for Treating AGE-Related Disease Us
:   TITLE OF INVENTION:  Inhibitors
:   FILE REFERENCE:  A-695
:   CURRENT APPLICATION NUMBER:  US/04/131,704
:   CURRENT FILING DATE:  2000-08-15
:   PRIOR APPLICATION NUMBER:  US 60/226,436
:   PRIOR FILING DATE:  2000-08-16
:   NUMBER OF SEQ ID NOS:  5
:   SOFTWARE:  Patent in version 3.1
:
: SEQ ID NO 1
:   LENGTH: 225
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   ORIGIN: 1-225
:   ORIGIN: 1-225

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Query Match 47.2% Score 34 DB 9 Length 225;
Best Local Similarity 72.4% Pred. NO. 114-C2;
Matches 5; Conservative 2; Mismatches 9; Indels

27	1 STOPPER
28	23 ALCOHOL 159

25017

US 09-011704-5
Sequence 5, Application US/09931704
Patent No. 052012041873A1
GENERAL INFORMATION:

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APPLICANT: NANTICO, INC.
TITLE OF INVENTION: Methods and Compositions for Treating ICG-related Disease US
PUBLICATION NO.: 2002/0051068
FILE REFERENCE: 2000/0014695
CURRENT APPLICATION NUMBER: US/09/953,704
CURRENT FILING DATE: 2001-09-17
PRIORITY APPLICATION NUMBER: US 60/226,435
PRIORITY FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTL version 3.3
SEQ ID NO: 5

```

LETTERS
TO THE EDITOR

ORGANISM. Marine.

every nation

Query Match: 57.2%; Score 34; DB 9; Length 425;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels

cy : SIGYLP ?
: : : :
cb : SIGYLP 159

RESULT 5
US 10-212-793-2
: Sequence 2: Application US/10212793
: Publication No. US201008739A

*** GENERAL INFORMATION ***

APPLICANT SINGAPORE CYCLOTRON

FILE REFERENCE: PF465D-1

CURRENT APPLICATION NUMBER: CS40/212,793

PRIOR APPLICATION NUMBER: US9/438,229

CURRENT FILING DATE: 2003-08-07

PRIOR FILING DATE: 1999-11-12

INVENTOR NAME: CHEN, JIAHONG

INVENTOR ADDRESS: 69/106,182

INVENTOR CITY: SINGAPORE

INVENTOR COUNTRY: SG

PRIOR APPLICATION NUMBER: US63/261,311

PRIOR FILING DATE: 1997-06-31

•

1 NUMBER OF SEQ ID NOS: 24
2 SEQ ID NO 2
3 LENGTH: 225
4 TYPE: PRT
5 ORGANISM: Homo sapiens
6 NAME/KEY: S1273
7 LOCATION: (225, 1)
8 FEATURE:
9 NAME/KEY: Pppl1p
10 LOCATION: (1), (158)
11 US-10-212-793-2

Query Match: 87.24; Score 34; DB 15; Length 225;
Best Local Similarity 71.44; Pred. No. 1, 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 S1273P 7
DB 153 AL52P1P 159

RESULT 6
US-09-864-761-7614
1 Sequence 37614, Application US/0984761
2 Patent No. US20020048753A1
3 GENERAL INFORMATION:
4 APPLICANT: Penn, Sharon G
5 INVENTOR: Penn, Sharon G
6 APPLICANT: Penn, Sharon G
7 APPLICANT: Penn, Sharon G
8 APPLICANT: Penn, Sharon G
9 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIDE AND PEPTIDES USEFUL IN MICROARRAY
10 FILE REFERENCE: Accmich-X-1
11 CURRENT APPLICATION NUMBER: US/09/564,761
12 PRIOR APPLICATION NUMBER: US 60/180,312
13 PRIOR FILING DATE: 2000-02-04
14 PRIOR APPLICATION NUMBER: US 60/207,456
15 PRIOR FILING DATE: 2000-03-06
16 PRIOR APPLICATION NUMBER: US 60/432,366
17 PRIOR FILING DATE: 2000-06-03
18 PRIOR APPLICATION NUMBER: GB 24263,4
19 PRIOR FILING DATE: 2000-10-04
20 PRIOR APPLICATION NUMBER: US 60/236,359
21 PRIOR FILING DATE: 2000-09-27
22 PRIOR APPLICATION NUMBER: PCT/US01/00666
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00667
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00664
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00669
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00665
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00668
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/00663
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: PCT/US01/00662
37 PRIOR FILING DATE: 2001-01-30
38 PRIOR APPLICATION NUMBER: PCT/US01/00660
39 PRIOR FILING DATE: 2001-01-30
40 PRIOR APPLICATION NUMBER: PCT/US01/00670
41 PRIOR FILING DATE: 2001-01-30
42 PRIOR APPLICATION NUMBER: US 60/234,657
43 PRIOR FILING DATE: 2000-09-21
44 PRIOR APPLICATION NUMBER: US 60/508,478
45 PRIOR FILING DATE: 2000-05-10
46 PRIOR APPLICATION NUMBER: US 60/774,203
47 PRIOR FILING DATE: 2001-01-25
48 NUMBER OF SEQ ID NOS: 4517

1 SOFTWARE: Amdotax Sequence Listing Engine vers. 1.1
2 SEQ ID NO: 37614
3 LENGTH: 17
4 TYPE: PRT
5 ORGANISM: Homo sapiens
6 NAME/KEY: S1273
7 LOCATION: (17, 1)
8 FEATURE:
9 NAME/KEY: Pppl1p
10 LOCATION: (1), (158)
11 US-09-364-761-7614

Query Match: 84.64; Score 33; DB 9; Length 17;
Best Local Similarity 71.44; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY 1 S1273P 7
DB 22 S1273P 24

RESULT 7
US-09-756-49-22
1 Sequence 22, Application US/075649
2 Patent No. US20020066710A1
3 GENERAL INFORMATION:
4 APPLICANT: Glucksmann, Maria A
5 INVENTOR: Glucksmann, Maria A
6 TITLE OF INVENTION: 20455, 579, 17134, 23821, 31894, and
7 FILE REFERENCE: US06/239272 US/06/755,694
8 CURRENT APPLICATION NUMBER: US/06/755,694
9 PRIOR APPLICATION NUMBER: US/06/755,694
10 PRIOR FILING DATE: 2000-12-29
11 NUMBER OF SEQ ID NOS: 42
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 22
14 LENGTH: 602
15 TYPE: PRT
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Pfam consensus sequence
19 US-09-755-695-22

Query Match: 84.54; Score 33; DB 9; Length 602;
Best Local Similarity 81.34; Pred. No. 4, 5e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 2 S1273P 7
DB 170 IG01P 175

RESULT 8
US-10-156-219-22
1 Sequence 22, Application US/0156239
2 Patent No. US2003036374A1
3 GENERAL INFORMATION:
4 APPLICANT: Glucksmann, Maria A
5 INVENTOR: Glucksmann, Maria A
6 TITLE OF INVENTION: NO. US2003036374A1 Nucleic Acid Sequences Encoding Human
7 FILE REFERENCE: AFAS010001, A Human Ubiquitin-Like Molecule,
8 TITLE OF INVENTION: AFAS010001, A Human Ubiquitin-Like Molecule,
9 TITLE OF INVENTION: AFAS010001, A Human Ubiquitin-Like Molecule,
10 FILE REFERENCE: US03/036374A1

1 PRIOR APPLICATION NUMBER: JP 2601-122125
 2 PRIOR FILING DATE: 2001-04-20
 3 NUMBER OF SEQ ID NOS: 22
 4 SEQ ID NO 10
 5 LENGTH: 927
 6 TYPE: PNT Human
 7 ORGANISM: HUMAN
 8 US-10-297-895A.10

Query Match 42.1% Score 32: DB 12 Length 427,
 Best Local Similarity 85.7% Pctd No. 11e-C3,
 Matches 6: Conservative C: Mismatches 1: Indels 0: Gaps 0:

Qy 1 SIGPEP 7
 Db 119 SIGPEP 135

RESULT 13

US-09-919-408-2
 1 Sequence 2: Application US/05W/0408
 2 Patent No. US2004072077A1
 3 GENERAL INFORMATION:
 4 APPLICANT: LAMARCA, JORGE R
 5 TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
 6 NUMBER OF SEQUENCES: 10
 7 ADDRESS: 180 VADICK STREET
 8 CITY: NEW YORK
 9 STATE: NEW YORK
 10 COUNTRY: U.S.A.
 11 ZIP: 10014

COMPUTER READABLE FORM:
 1 MEDIUM TYPE: floppy disk
 2 COMPUTER: IBM PC COMPATIBLE
 3 OPERATING SYSTEM: PC DOS/MS-DOS
 4 SOFTWARE: PATENT RELEASE #1.0, Version #1.25
 5 CURRENT APPLICATION DATA: US/09/719,418
 6 FILING DATE: 11-JUL-2001

CLASSIFICATION: <Unknown>
 1 APPLICATION NUMBER: 07/977,451
 2 FILING DATE: 26-JUN-1992
 3 APPLICATION NUMBER: US 07/906,397
 4 FILING DATE: 26-JUN-1992
 5 APPLICATION NUMBER: US PCT/US92/05401
 6 FILING DATE: 26-JUN-1992
 7 APPLICATION NUMBER: 1102951
 8 FILING DATE: 15-APR-1992
 9 APPLICATION NUMBER: US PCT/US92/02750
 10 FILING DATE: 02-APR-1992
 11 APPLICATION NUMBER: US 07/813,593
 12 FILING DATE: 24-DEC-1991
 13 APPLICATION NUMBER: US 07/793,365
 14 FILING DATE: 15-NOV-1991
 15 APPLICATION NUMBER: US 07/728,913
 16 FILING DATE: 28-JUN-1991
 17 APPLICATION NUMBER: US 07/679,666
 18 FILING DATE: 03-APR-1991

ATTORNEY/AGENT INFORMATION:
 1 NAME: FELT, IVINS N.
 2 REGISTRATION NUMBER: 28,601
 3 REFERENCE/DOCKET NUMBER: LEM-1-7P
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: 212-645-1405
 6 TELEFAX: 212-645-2054
 7 INFORMATION FOR SEQ ID NO: 2:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 992 amino acids
 10 TYPE: amino acid

1 Molecule Type: PNTail
 2 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 3 US-09-919-408-2

Query Match 82.1% Score 32: DB 9 Length 592,
 Best Local Similarity 85.7% Pctd No. 11e-C3,
 Matches 9: Conservative C: Mismatches 1: Indels 0: Gaps 0:

Qy 1 SIGPEP 7
 Db 456 SIGPEP 481

RESULT 14

US-09-872-115-2
 1 Sequence 2: Application US/09/272,336
 2 Patent No. US2003013545A2
 3 GENERAL INFORMATION:
 4 APPLICANT: JODROVSKY, JORGE R
 5 TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
 6 NUMBER OF SEQUENCES: 10
 7 ADDRESS: 180 VADICK STREET
 8 CITY: NEW YORK
 9 STATE: NEW YORK
 10 COUNTRY: U.S.A.
 11 ZIP: 10014

COMPUTER READABLE FORM:
 1 MEDIUM TYPE: floppy disk
 2 COMPUTER: IBM PC COMPATIBLE
 3 OPERATING SYSTEM: PC DOS/MS-DOS
 4 SOFTWARE: PATENT RELEASE #1.0, Version #1.25
 5 CURRENT APPLICATION DATA: US/09/872,116
 6 FILING DATE: 01-JUN-2001

CLASSIFICATION: <Unknown>
 1 APPLICATION NUMBER: 09/09208,786
 2 FILING DATE: <Unknown>
 3 APPLICATION NUMBER: 09/092,124
 4 FILING DATE: <Unknown>
 5 APPLICATION NUMBER: 09/077,451
 6 FILING DATE: 15-APR-1992
 7 APPLICATION NUMBER: US 07/906,397
 8 FILING DATE: 26-JUN-1992
 9 APPLICATION NUMBER: US PCT/US92/05401
 10 FILING DATE: 26-JUN-1992
 11 APPLICATION NUMBER: 1102951
 12 FILING DATE: 15-APR-1992
 13 APPLICATION NUMBER: US PCT/US92/02750
 14 FILING DATE: 02-APR-1992
 15 APPLICATION NUMBER: US 07/813,593
 16 FILING DATE: 24-DEC-1991
 17 APPLICATION NUMBER: US 07/793,365
 18 FILING DATE: 15-NOV-1991
 19 APPLICATION NUMBER: US 07/728,913
 20 FILING DATE: 28-JUN-1991
 21 APPLICATION NUMBER: US 07/679,666
 22 FILING DATE: 03-APR-1991

ATTORNEY/AGENT INFORMATION:
 1 NAME: FELT, IVINS N.
 2 REGISTRATION NUMBER: 28,601
 3 REFERENCE/DOCKET NUMBER: LEM-3-7P
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: 212-645-1405
 6 TELEFAX: 212-645-2054
 7 INFORMATION FOR SEQ ID NO: 2:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 992 amino acids
 10 TYPE: amino acid

Result	Score	Query Match	Length	CB	ID	Description
1	38	97.4	1064	2	I38074	hypothetical protein
2	37	94.9	602	2	A81654	conserved hypothetical
3	36	92.3	208	2	Q74406	serine protease
4	35	89.7	239	2	B88967	probable proteinase A
5	34	87.2	530	2	Q32061	conserved hypothetical
6	34	87.2	760	2	D56465	hypothetical protein
7	34	87.2	1611	2	I38216	hypothetical protein
8	33	84.6	227	2	B87118	probable uracil-DNA
9	33	84.6	227	2	I50672	membrane transporter
10	33	84.6	537	2	I34964	vesicle-membrane
11	33	84.6	514	2	B28910	probable regulator
12	33	84.6	515	2	A46372	hypothetical protein
13	33	84.6	517	2	S41581	monomeric transporter
14	33	94.6	614	2	A46385	RNA polymerase
15	33	84.5	514	2	O71082	transporter
16	33	84.6	982	2	A53551	hypothetical protein
17	33	84.6	818	2	I51920	conserved hypothetical
18	33	84.6	2819	2	A90551	probable RNA polymerase
19	33	84.6	3157	2	Q70969	hypothetical protein
20	32	82.1	209	2	G50445	probable signal peptidase
21	32	82.1	269	2	A72597	proteinase
22	32	82.1	191	2	B93668	hypothetical protein
23	32	82.1	191	2	S75553	hypothetical protein
24	32	82.1	422	2	O71192	hypothetical protein
25	32	82.1	424	2	A70556	epithelial protein
26	32	82.1	445	2	A70556	hypothetical protein
27	32	82.1	507	2	Q26809	q-mannosidase
28	32	82.1	513	1	B26191	q-mannosidase

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57	57	57	57	57	57
58	58	58	58	58	58
59	59	59	59	59	59
60	60	60	60	60	60
61	61	61	61	61	61
62	62	62	62	62	62
63	63	63	63	63	63
64	64	64	64	64	64
65	65	65	65	65	65
66	66	66	66	66	66
67	67	67	67	67	67
68	68	68	68	68	68
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71	71	71	71	71	71
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73	73	73	73	73	73
74	74	74	74	74	74
75					

submitted to the EMBL Data Library, February 1999

A:Reference number: 221780
 A:Accession: FJ8236
 A>Status: Preliminary: translated from Gb/EMBL/DBNC
 A:Molecule type: DNA
 A:Cross-references: EMBL:ALC21813, PDB:1AAL49s1.1, GSPDB:GN00046, SPCB:SPAC23A1.17
 A:Experimental source: strain 912N; consaid c23A;
 C:Genetics:
 A:Gene: SPDB:SPAC23A1.17
 A:Map position: 1

Query Match 87.24; Score 34; DB 2; Length 1611;
 Best Local Similarity 85.74; Pred. No. 21e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 STGYPG 7
 DB 834 STGHPG 440

RESULT 8

uracil-DNA glycosylase ung [Imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-1999 #sequence_revision 20-Apr-2002 #text_change 10-May-03
 C:Accession: S29610
 R:Colles, S.T., Eigemeier, K., Parish, J., James, K.D., Thomson, K., Whitehead, S., Squares, S., Davies, M., Davies, K.M., Devlin, K., Dutley, S., Feltwell, D., Fraser, A., Hartley, N., Heirys, E., M.A., Rutherford, K.M., Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S., Seeger, K., Simon, S., Stanouds, M., Skelton, J., Squares, S., Gordon, E., Whitehead, S., Davies, K., Devlin, K., Feltwell, D., Gentles, S., Hartley, N., Eigemeier, S., Colles, S.T., Eigemeier, K., Parish, J., James, K.D., Thomson, K., Whitehead, S., Squares, S., Davies, M., Davies, K.M., Devlin, K., Dutley, S., Feltwell, D., Fraser, A., Hartley, N., Heirys, E., M.A., Rutherford, K.M., Nature 409, 1007-1011, 2001
 A:Title: Massive gene decay in the leprosy bacillus
 A:Reference number: AB5509; M01D:2126732; PMID:11234032
 A:Accession: E57116
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Cross-references: EMBL:AL453380; NID:q109443; PDB:1AC10628.1; GSPDB:GN000447
 C:Genetics:
 A:Gene: ung
 C:Superfamily: uracil-DNA glycosylase

Query Match 84.64; Score 33; DB 2; Length 227;
 Best Local Similarity 83.34; Pred. No. 41;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 2 LGYPLP 7
 DB 105 LGYPLP 110

RESULT 9

probable uracil-DNA glycosylase - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1995 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: E70672
 R:Cole, S.T., Brosch, P., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S., Connor, R., Davies, K., Devlin, K., Feltwell, T., Gentles, S., Hartley, N., Eigemeier, S., Colles, S.T., Eigemeier, K., Parish, J., James, K.D., Thomson, K., Whitehead, S., Squares, S., Davies, M., Davies, K.M., Devlin, K., Dutley, S., Feltwell, D., Fraser, A., Hartley, N., Heirys, E., M.A., Rutherford, K.M., Nature 409, 1007-1011, 2001
 A:Authors: Squares, S., Sulston, J.E., Taylor, K., Whitehead, S., Hartley, N., G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; M01D:9829587; PMID:9634230
 A:Accession: E70672
 A>Status: Preliminary: nucleic acid sequence not shown.
 A:Molecule type: DNA
 A:Residues: 1-227 <COL>
 A:Cross-references: GB:283028; GB:AL23456; NID:q326167; PDB:1AC10628.1; FID:q1694855
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: ung

C:Superfamily: uracil-DNA glycosylase

Query Match 84.64; Score 33; DB 2; Length 227;
 Best Local Similarity 83.34; Pred. No. 41;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 2 LGYPLP 7
 DB 105 LGYPLP 110

RESULT 10

probable regulatory protein - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C:Accession: S29610
 R:Colles, S.T., Eigemeier, K., Parish, J., James, K.D., Thomson, K., Whitehead, S., Squares, S., Davies, M., Davies, K.M., Devlin, K., Dutley, S., Feltwell, D., Fraser, A., Hartley, N., Heirys, E., M.A., Rutherford, K.M., Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S., Seeger, K., Simon, S., Stanouds, M., Skelton, J., Squares, S., Gordon, E., Whitehead, S., Davies, K., Devlin, K., Feltwell, D., Gentles, S., Hartley, N., Eigemeier, S., Colles, S.T., Eigemeier, K., Parish, J., James, K.D., Thomson, K., Whitehead, S., Squares, S., Davies, M., Davies, K.M., Devlin, K., Dutley, S., Feltwell, D., Fraser, A., Hartley, N., Heirys, E., M.A., Rutherford, K.M., Nature 409, 1007-1011, 2001
 A:Title: Massive gene decay in the leprosy bacillus
 A:Reference number: AB5509; M01D:2126732; PMID:11234032
 A:Accession: E57116
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Cross-references: EMBL:AL453380; NID:q109443; PDB:1AC10628.1; GSPDB:GN000447
 C:Genetics:
 A:Gene: ung
 C:Superfamily: uracil-DNA glycosylase

Query Match 84.64; Score 33; DB 2; Length 137;
 Best Local Similarity 84.74; Pred. No. 43;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 STGYPG 7
 DB 172 STGHPG 136

RESULT 11

moraxine transport protein - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
 C:Accession: S29610
 R:Stratton, C.K., Persico, A.M., Vand, X.D., Edgar, S.K., Bird, G.S., Hawkins, A.L., PMS 666, 318, 325-330, 1993
 A:Title: A human synaptic vesicle acetylcholine transporter cDNA predicts posttranslat.
 A:Reference number: 221563
 A:Accession: S29610
 A>Status: Preliminary
 A:Molecule type: cDNA
 A:Residues: 1-514 <STR>
 A:Cross-references: GB:L05118; NID:3262334; PDB:AAA59877.1; FID:q292315
 C:Superfamily: synaptic vesicle amino transporter
 C:Keywords: transmembrane protein

Query Match 84.54; Score 33; DB 2; Length 514;
 Best Local Similarity 83.34; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 2 LGYPLP 7
 DB 155 LGYPLP 161

RESULT 12

vesicle monoamine transporter - human
 A:Accession: A49468
 N:Accession names: amino transporter, brain synaptic vesicle
 C:Species: Homo sapiens (man)
 C:Date: 26-May-1998 #sequence_revision 12-May-1995 #text_change 17-Nov-2000
 C:Accession: A49468; JN0022; I19261; S32766

R.Peter, D.; Finn, J.P.; Kisek, I.; Liu, Y.; Kojia, T.; Hozomura, O.; Rahmati, A.; Spd
Genetics 16, 720-723, 1993
A:Accession: A4368; NCID:9414368; PMID:7505809
A:Reference: A4368; NCID:9414368; PMID:7505809
A:Status: Preliminary; nucleic acid sequence not shown, not compared with nonredundant
A:Molecule type: mRNA
A:Residues: 1-514 <ERR>
P.Erickson, J.D.; Eiden, L.E.
J. Neurochem. 61, 2314-2317, 1993
A:Title: Functional identification and molecular cloning of a human brain vesicular monoamine
A:Reference number: JN5825; NCID:9406582; PMID:8454583
A:Accession: A4368; NCID:9414368; PMID:7505809
A:Residues: 1-514 <ERR>
A:Cross-references: GB:U23205; NCID:9434971; PID:AA61290.1; PID:9434971
R.Lesch, K.P.; Gross, J.; Wolozin, B.L.; Murphy, D.L.; Riederer, P.
J. Neural Transm. 93, 75-82, 1994
A:Title: Extensive sequence divergence between the human and rat brain vesicular monoamine
A:Reference number: 139221
A:Accession: 139221
A:Molecule type: mRNA
A:Status: preliminary; translated from GU/EMBL/DBJ
A:Residues: 1-516, H, 18-514 <RUS>
A:Cross-references: EMBL:X71554; NCID:926488; PID:CA55046.1; PID:926488
A:Accession: A4368; NCID:9414368; PMID:7505809
A:Status: Preliminary; This protein allows neurotransmitters to be accumulated from the cytor.asm in
A:Gene: VMAT2; VMT2; SVAT
A:Map position: 10q25
C:Superfamily: synaptic vesicle amine transporter
C:Keywords: glycoprotein; phosphoprotein; transmembrane protein
F121-44/Domain: transmembrane status predicted <TM>
F130-151/Domain: transmembrane status predicted <TM>
F160-179/Domain: transmembrane status predicted <TM>
F190-210/Domain: transmembrane status predicted <TM>
F292-311/Domain: transmembrane status predicted <TM>
F328-352/Domain: transmembrane status predicted <TM>
F358-378/Domain: transmembrane status predicted <TM>
F388-410/Domain: transmembrane status predicted <TM>
F417-437/Domain: transmembrane status predicted <TM>
F446-470/Domain: transmembrane status predicted <TM>
F15.18.279/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted
F153.496/Binding site: phosphate (Thr) (covalent) (by protein kinase A) status predicted
F416/Binding site: phosphate (Ser) (covalent) (by protein kinase A) status predicted
Query Match 84.6%; Score 33; DB 2; Length 514;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 ICYPLP 7
DB 159 ICYPLP 16;
RES027 13
A46374
A:Title: Rat vesicular monoamine transporter - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Sep-1993; sequence revision 19-Nov-1994; text change 17 Nov 2003
C:Accession: A46374; B43319; text change 17 Nov 2003
P.Erickson, J.D.; Eiden, L.E.; Hoffman, B.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 10993-10997, 1989
A:Title: Expression cloning of a reserpine-sensitive vesicular monoamine transporter
A:Reference number: A46374; NCID:94066170; PMID:1436194
A:Accession: A46374
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-515 <ERR>
A:Cross-references: NCID:9406582; NCID:9434971; PID:AA61290.1; PID:9434971
A:Residues: 1-515 <ERR>
R.Liu, Y.; Peter, D.; Rahmati, A.; Schindler, S.; Priyo, G.G.; Fischberg, D.; Hozomura, N.
Cell 70, 539-551, 1992

A:Title: A cDNA that suppresses MPP+ toxicity encodes a vesicular amine transporter
A:Accession: A46374; NCID:94066170; PMID:1505025
A:Reference: A46374; NCID:94066170; PMID:1505025
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-515, K, 22-515, L, 20-515
A:Title: Sequence extracted from MPP+ backbone (NCBI:114157, NCBI:114158)
A:Note: Sequence extracted from MPP+ backbone (NCBI:114157, NCBI:114158)
C:Superfamily: synaptic vesicle amine transporter
Query Match 84.6%; Score 33; DB 2; Length 515;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 ICYPLP 7
DB 159 ICYPLP 16;
RES027 14
S41261
A:Title: monoamine transport protein 2, vesicular - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 25-Dec-1994; sequence revision 05-Apr-1995; text change 24-Sep-1993
A:Accession: S41261; S39440; S39441; A42055
A:Reference number: S39440; NCID:94063073; PMID:7902299
A:Title: Cloning and functional expression of a tetrahydrozine sensitive vesicular m
A:Reference number: S41261; NCID:94063073; PMID:7902299
A:Accession: S41261
A:Molecule type: mRNA
A:Residues: 1-517 <RUS>
A:Cross-references: GB:U23205; NCID:9434971; PID:AA61290.1; PID:9434971
A:Experimental source: adrenal medulla
R.Krejci, P.; Gagliardi, B.; Bottom, D.; Isambert, M.F.; Sayne, C.; Gagnon, J.; Masson
Proc. Natl. Acad. Sci. U.S.A. 89, 9730-9734, 1992
A:Title: Expression and regulation of the bovine vesicular monoamine transporter ge
A:Reference number: S39440; NCID:94063073; PMID:7902299
A:Accession: S39440
A:Molecule type: mRNA
A:Residues: 1-527, T, 54-181, S, 155-464, S, 466, F, 467-473, SRS, 477-517 <KRE>
A:Cross-references: GB:U23205; NCID:9434971; PID:AA61290.1; PID:9434971
A:Accession: S39441
A:Molecule type: protein
A:Residues: 2-4, X, 16-5; XX, 12-13, 36-49, X, 51-52, XX, 55, X, 180-182, XS, 185-197
A:Experimental source: adrenal medulla
R.Krejci, P.; Gagliardi, B.; Bottom, D.; Isambert, M.F.; Sayne, C.; Gagnon, J.; Masson
Proc. Natl. Acad. Sci. U.S.A. 89, 9730-9734, 1992
A:Title: Homology of a vesicular amine transporter to a gene conferring resistance
A:Reference number: A47205; NCID:93286316; PMID:1357568
A:Accession: A47205
A:Molecule type: protein
A:Residues: 3-13, X, 21-28, X, 30-294-295, C, 297-300, K, 302 <STE>
A:Experimental source: adrenal medulla
A:Note: sequence modified after extraction from MPP+ backbone
C:Superfamily: synaptic vesicle amine transporter
C:Keywords: glycoprotein; membrane protein
Query Match 84.6%; Score 33; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 ICYPLP 7
DB 159 ICYPLP 16;
RES027 15
S41261
A:Title: RNA helixase TM2 - mouse
A:Accession: S41261
A:Residues: 1-514 <ERR>
A:Cross-references: NCID:9406582; NCID:9434971; PID:AA61290.1; PID:9434971
A:Residues: 1-514 <ERR>
A:Title: Sequence extracted from MPP+ backbone (NCBI:114157, NCBI:114158)
A:Note: Sequence extracted from MPP+ backbone (NCBI:114157, NCBI:114158)
C:Superfamily: synaptic vesicle amine transporter

C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 (sequence revision 10-Sep-1999) atext_cchange 19-Jan-2001
C:Accession: I48385; S21453
C:Definition: Mus musculus nucleotide-binding motif A.
C:Features: 12, 68-106, 109-110, 113-114, 117-118, 121-122, 125-126, 129-130, 133-134, 137-138, 141-142, 145-146, 149-150, 153-154, 157-158, 161-162, 165-166, 169-170, 173-174, 177-178, 181-182, 185-186, 189-190, 193-194, 197-198, 201-202, 205-206, 209-210, 213-214, 217-218, 221-222, 225-226, 229-230, 233-234, 237-238, 241-242, 245-246, 249-250, 253-254, 257-258, 261-262, 265-266, 269-270, 273-274, 277-278, 281-282, 285-286, 289-290, 293-294, 297-298, 301-302, 305-306, 309-310, 313-314, 317-318, 321-322, 325-326, 329-330, 333-334, 337-338, 341-342, 345-346, 349-350, 353-354, 357-358, 361-362, 365-366, 369-370, 373-374, 377-378, 381-382, 385-386, 389-390, 393-394, 397-398, 401-402, 405-406, 409-410, 413-414, 417-418, 421-422, 425-426, 429-430, 433-434, 437-438, 441-442, 445-446, 449-450, 453-454, 457-458, 461-462, 465-466, 469-470, 473-474, 477-478, 481-482, 485-486, 489-490, 493-494, 497-498, 501-502, 505-506, 509-510, 513-514, 517-518, 521-522, 525-526, 529-530, 533-534, 537-538, 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985-986, 989-990, 993-994, 997-998, 1001-1002, 1005-1006, 1009-1010, 1013-1014, 1017-1018, 1021-1022, 1025-1026, 1029-1030, 1033-1034, 1037-1038, 1041-1042, 1045-1046, 1049-1050, 1053-1054, 1057-1058, 1061-1062, 1065-1066, 1069-1070, 1073-1074, 1077-1078, 1081-1082, 1085-1086, 1089-1090, 1093-1094, 1097-1098, 1101-1102, 1105-1106, 1109-1110, 1113-1114, 1117-1118, 1121-1122, 1125-1126, 1129-1130, 1133-1134, 1137-1138, 1141-1142, 1145-1146, 1149-1150, 1153-1154, 1157-1158, 1161-1162, 1165-1166, 1169-1170, 1173-1174, 1177-1178, 1181-1182, 1185-1186, 1189-1190, 1193-1194, 1197-1198, 1201-1202, 1205-1206, 1209-1210, 1213-1214, 1217-1218, 1221-1222, 1225-1226, 1229-1230, 1233-1234, 1237-1238, 1241-1242, 1245-1246, 1249-1250, 1253-1254, 1257-1258, 1261-1262, 1265-1266, 1269-1270, 1273-1274, 1277-1278, 1281-1282, 1285-1286, 1289-1290, 1293-1294, 1297-1298, 1301-1302, 1305-1306, 1309-1310, 1313-1314, 1317-1318, 1321-1322, 1325-1326, 1329-1330, 1333-1334, 1337-1338, 1341-1342, 1345-1346, 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DR EMBL: L23205; AA61290.1; 1.
DR EMBL: L14269; AA91851.1; 1.
DR EMBL: X71354; CA50459.1; 1.
DR PIR: A49365; A49368.
DR CAC: S29810; S29816; SL1882.
DR MW: 19320; C13935; SL1882.
DR GO: GO:0005687; C: integral to plasma membrane; IAS.
DR GO: GO:0003624; C: membrane fraction; TAS.
DR GO: GO:0005803; C: secretory vesicle; TAS.
DR GO: GO:0008504; F: monoamine transporter activity; TAS.
DR GO: GO:0015844; F: monoamine transport; TAS.
DR InterPro: IPR007114; NES.
KW Transport; Transmembrane; Glycoprotein; Neurotransmitter transport;
KW Phosphorylation; 1 20 CYTOPLASMIC (POTENTIAL);
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 21 42 POTENTIAL LUMEN (POTENTIAL);
FT TRANSMEM 43 170 POTENTIAL;
FT TRANSMEM 130 150 POTENTIAL;
FT DOMAIN 151 159 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 160 180 POTENTIAL;
FT DOMAIN 181 189 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 190 210 POTENTIAL;
FT DOMAIN 211 219 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 220 242 POTENTIAL;
FT DOMAIN 243 248 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 249 271 POTENTIAL;
FT DOMAIN 272 291 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 292 312 POTENTIAL;
FT DOMAIN 313 352 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 353 357 CYTOPLASMIC (POTENTIAL);
FT DOMAIN 358 378 POTENTIAL;
FT TRANSMEM 379 389 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 390 410 POTENTIAL;
FT DOMAIN 411 414 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 415 435 POTENTIAL;
FT DOMAIN 436 440 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 441 462 POTENTIAL;
FT DOMAIN 463 514 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 515 544 POTENTIAL;
FT CARBOHYD 84 84 N-LINKED (GLCNAc 1) (POTENTIAL);
FT MOD_RES 511 511 PHOSPHORYLATION (BY CK2) (BY SIMILARITY);
FT MOD_RES 513 513 PHOSPHORYLATION (BY CK2) (BY SIMILARITY);
FT CONFLICT 17 17 R -> H (IN REF. 1);
FT CONFLICT 302 302 C -> S (IN REF. 1);
FT CONFLICT 354 354 K -> T (IN REF. 1);
FT CONFLICT 378 378 A -> P (IN REF. 1);
FT CONFLICT 395 395 I -> N (IN REF. 1);
FT CONFLICT 514 514 I -> N (IN REF. 1);
SQ SEQUENCE 514 AA: 55712 MW: 42541425485082 CRC64:
Query Match: 84.6% Score 33; DB 1; Length 514;
Best Local Similarity: 81.3% Pred. No. 579
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
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Db 156 IGVPEP 161
RESULT 7
1072127
AC Q01877 STANDARD. PRT: 515 AA.
DI 01-JUL-1993 (Rel. 26, last sequence update)
DI 01-JUL-1993 (Rel. 26, last sequence update)
DI 28-FEB-2003 (Rel. 41, last annotation update)
DE Synaptic vesicle amine transporter (Monoamine transporter) (Wistar)
DE amine transporter 2) (VA-2)
GN SL18A2 OR VMAT2 OR VMAT
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Manali; Eukarya; Metazoa; Craniata; Vertebrata; Euteleostomi;
CC NCBI_TaxID: 10116;
CC [1]
CC SEQUENCE FROM N.A.
CC METCINE-9270677; PIRNA-150422;
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC FA CNA that suppresses MEPA toxicity encodes a vesicular amine
CC transporter.*;
CC Q-1: 70-535-553(1492);
CC [2]
CC SEQUENCE FROM N.A.
CC METCINE-9270677; PIRNA-150422;
CC FRICKSON J.D., EDEL L.E., HOFFMAN B.J.
CC Expression cloning of a reserpine-sensitive vesicular monoamine
CC transporter.*;
CC Proc. Natl. Acad. Sci. U.S.A. 89:10593-10597(1992);
CC PHOSPHORYLATION OF SER-512 AND SER-514
CC MDLNE-9270677; PIRNA-150422;
CC KRAVITZ D.E., PETER D., LUI Y., EDWARDS R.H.
CC "Phosphorylation of a vesicular monoamine transporter by casein
CC kinase II".
CC J. Biol. Chem. 272:6752-6759(1997);
CC - FUNCTION: INVOLVED IN THE ATP-DEPENDENT VESICULAR TRANSPORT OF
CC BIOGENIC AMINE NEUROTRANSMITTERS. REQUISITE FOR VESICULAR AMINE
CC STORAGE PRIOR TO SECRETION VIA EXOCYTOSIS.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VESICULAR
CC - MEMBRANE SPECIFICITY: BRAINSTEM AND STOMACH
CC - SIMILARITY: STRONG WITH CHROMATIN GRANULE AMINE TRANSPORTER AND
CC TO INVERTEBRATE VESICULAR ACETYLCHOLINE TRANSPORTER.
CC
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CC [1]
CC EMBL: M97351; AA42190.1; 1.
CC PIR: A46374; A46374.
CC InterPro: IPR007114; NES.
KW Transport; Transmembrane; Glycoprotein; Neurotransmitter transport;
KW Phosphorylation; 1 20 CYTOPLASMIC (POTENTIAL);
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FT TRANSMEM 21 42 POTENTIAL;
FT DOMAIN 43 130 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 131 152 POTENTIAL;
FT DOMAIN 153 180 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 182 190 VESICULAR LUMEN (POTENTIAL);
FT DOMAIN 192 210 POTENTIAL;
FT TRANSMEM 211 220 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 221 243 POTENTIAL;
FT DOMAIN 244 249 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 250 272 POTENTIAL;
FT DOMAIN 273 292 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 293 314 VESICULAR LUMEN (POTENTIAL);
FT DOMAIN 315 325 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 326 353 VESICULAR LUMEN (POTENTIAL);
FT DOMAIN 354 379 POTENTIAL;
FT TRANSMEM 380 392 VESICULAR LUMEN (POTENTIAL);
FT DOMAIN 393 415 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 416 426 POTENTIAL;
FT DOMAIN 427 441 VESICULAR LUMEN (POTENTIAL);
FT TRANSMEM 442 463 POTENTIAL;
FT DOMAIN 464 515 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 516 525 BY SIMILARITY.

CR	InterPro: IPR015928, Sub_transporter.
DR	Plan: PF00033: Aaak.ct: 1.
KW	Transp. Transmembrane. Glycoprotein: Neurotransmitter transport.
FT	FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN 21 41 POTENTIAL.
FT	DOMAIN 42 142 VESICULAR LUMEN (POTENTIAL).
FT	TRANSMEN 133 153 POTENTIAL.
FT	DOMAIN 154 162 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN 163 183 POTENTIAL.
FT	DOMAIN 184 192 VESICULAR LUMEN (POTENTIAL).
FT	TRANSMEN 193 213 POTENTIAL.
FT	DOMAIN 214 222 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN 223 243 POTENTIAL.
FT	DOMAIN 244 252 VESICULAR LUMEN (POTENTIAL).
FT	TRANSMEN 253 274 POTENTIAL.
FT	DOMAIN 275 294 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN 295 314 POTENTIAL.
FT	DOMAIN 315 331 VESICULAR LUMEN (POTENTIAL).
FT	TRANSMEN 332 355 POTENTIAL.
FT	DOMAIN 356 363 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN 364 382 POTENTIAL.
FT	DOMAIN 383 392 VESICULAR LUMEN (POTENTIAL).
FT	TRANSMEN 393 414 POTENTIAL.
FT	DOMAIN 415 437 POTENTIAL.
FT	TRANSMEN 438 438 POTENTIAL.
FT	DOMAIN 439 443 VESICULAR LUMEN (POTENTIAL).
FT	TRANSMEN 444 465 POTENTIAL.
FT	DOMAIN 466 477 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEN 478 517 BY SIMILARITY.
FT	DOMAIN 518 527 N-LINKED GLCNAC. (3 POTENTIAL).
FT	TRANSMEN 528 547 N-LINKED GLCNAC. (3 POTENTIAL).
FT	DOMAIN 548 567 N-LINKED GLCNAC. (3 POTENTIAL).
FT	TRANSMEN 568 587 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
FT	DOMAIN 588 607 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
FT	TRANSMEN 608 627 A -> I (IN REF. 2).
FT	DOMAIN 628 647 I -> S (IN REF. 2).
FT	TRANSMEN 648 667 A -> S (IN REF. 2).
FT	DOMAIN 668 687 L -> SF (IN REF. 2).
FT	TRANSMEN 688 707 RSP -> SKS (IN REF. 2).
FT	DOMAIN 708 727 RSP -> SKS (IN REF. 2).
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FT	DOMAIN 748 767 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 768 787 RSP -> SKS (IN REF. 2).
FT	DOMAIN 788 807 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 808 827 RSP -> SKS (IN REF. 2).
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FT	DOMAIN 908 927 RSP -> SKS (IN REF. 2).
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FT	DOMAIN 1188 1207 RSP -> SKS (IN REF. 2).
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FT	TRANSMEN 1248 1267 RSP -> SKS (IN REF. 2).
FT	DOMAIN 1268 1287 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 1288 1307 RSP -> SKS (IN REF. 2).
FT	DOMAIN 1308 1327 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 1328 1347 RSP -> SKS (IN REF. 2).
FT	DOMAIN 1348 1367 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 1368 1387 RSP -> SKS (IN REF. 2).
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FT	TRANSMEN 1448 1467 RSP -> SKS (IN REF. 2).
FT	DOMAIN 1468 1487 RSP -> SKS (IN REF. 2).
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FT	DOMAIN 1548 1567 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 1568 1587 RSP -> SKS (IN REF. 2).
FT	DOMAIN 1588 1607 RSP -> SKS (IN REF. 2).
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FT	DOMAIN 1948 1967 RSP -> SKS (IN REF. 2).
FT	TRANSMEN 1968 1987 RSP -> SKS (IN REF. 2).
FT	DOMAIN 1988 20

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DR   DQ: GC0936645; Prol-1 growth; RAS.  

DS   InterPro: PR000627; DEAC_Box  

DS   InterPro: PR000628; DEAC_Box  

DS   InterPro: PR000630; Helicase_C.  

DS   Pfam: PF00270; DEAD_1  

DS   Pfam: PF00271; Helicase_C_1  

DS   SMART: SMC0487; HELIC_1  

DS   SMART: SMC0490; DEAD_1  

DS   PROSITE: PS00349; DEAC-ATP_Helicase...  

KW   ATP-binding, RNA-binding; Helicases, Nuclear protein,  

SE   BINDING, NUCLEAR, SIMILARITY.  

ST   EMBL 248    251  

SQ     SEQUENCE 214 AA: 5514R MW: 84095847D601594 CRG54;  

      Query Match          P4 63: SecE 33: DB 1: Length 614:  

      Best Local Similarity 61.3% Pred No. 50:  

      Matches 5; Conservative 12 Mismatches 0; Indels 0; Gaps 0;  

OY       2 COMPLET ?              11111  

DC       614 COMPACT +C+

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RESULTS C  

ID DEX5_MOUSE STANDARD. PROT. 614 AA.  

AC Q67656.  

DI G1 NOV-1997 (Ref. seq. treated)  

DI G1 NOV-1997 (Ref. seq. last annotation update)  

DI 16 JUL 2003 (Ref. seq. last annotation update)  

DI 01 DEC 2003 (Ref. seq. last annotation update) NCBI  

UN CD00245 DEAC-box PNA Helicase DEAC17 (DEAD1).  

GN LOC506187 DEAC-box PNA Helicase DEAC17 (DEAD1).  

OS Mus musculus (Mus.)  

CC Buxarroya, Velazquez; Chabutti; Criblata, Verbitratia; Euteleostomi;  

CC Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  

CX MARRA1B-Taxid:100340;  

CX [ ]  

RN SEQUENCE FROM N.A. TISSUE-CULTURE  

RP EXPRESSION PATTERNS: FETUS, ADULT  

RA MIMMELNBERG1466; TISSUE=H443/H98;  

BA Legendre L., Heliogut J.A.B.  

RT *Peak level expression in male germ cells of murine p68 RNA helicase  

FC  

KL Lit. Acc. Z2517-145(1993);  

CC FUNCTION: RNA DEPENDENT ATPASE ACTIVITY. THE RATE OF ATP  

CC HYDROLYSIS IS HIGHLY STIMULATED BY SINGLE-STRAWED RNA (BY  

CC SIMILARITY).  

CC SUBCELLULAR LOCATION: Nucleus (By similarity)  

CC : BELONGS TO THE DEAD BOX HELICASE FAMILY. DDX5/DDX17  

CC SUBFAMILY.

```

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EMBL: X65627; CBAB4581.1;  

ZEB: A33185; I42935;  

KSSP: QA6054; HVV5.  

NCBI: MG113637; Ddx5.  

InterPro: IPROC1470; DEAD.  

TrinE-Pro: TRPC00629; DEAD_Box.  

InterPro: IPROC0629; DEAD_Box.  

Pfam: PF00270; DEAD_1.  

SMART: SMC0487; Helicase_C_1;  

SMART: SMC0490; DEAD_1  

PROSITE: PS00349; DEAC-ATP_Helicase_1.  

HYDROLASE, ATP-BINDING, HELICASE, RNA-BINDING, Nuclear protein.
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[illegible]

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CC EXHL IC2594; AAAS59262;
CC EXHL IC2595; AAGS59263;
CC EXHL IC2596; AAGS59264;
CC DR PIP_ B26149; B26100;
CC DR Sub-List; B31C649; gntK;
CC DR InterPro; IPR003577; FGXY kin;
CC DR InterPro; IPR003602; Glucuronate kinase
CC Dran; FCUJ782; FGXY_C_1;
CC DR Pfam; PF07792; FGXY_C_1;
CC DR Pfam; PF07792; FGXY_C_1;
CC DR SIGFAM5; TIGR01114; gntK_FGXY_1;
CC DR SIGFAM5; TIGR01114; gntK_FGXY_2;
CC DR PRESITE; PS00919; FGXY_K_NA2E_1;
CC DR PRESITE; PS00919; FGXY_K_NA2E_1;
CC DR GLUCURONATE UTILZAT100; Transferrase; Kinase; Complete proteome.
CC SEQUNCE; 513 AA; 57455 MW; 35.D04:04-47AC3ED CRC64;
CC
CC Query Match 82.1%; Score 32; CB.L; Length 513;
CC Best Local Similarity; 100 CA; Pred.No. 78;
CC Matches Conservative C; Mismatches C; Indels G; Gaps
CC
CC 2Y 1 NRYTL 5
CC 31 NRYPL 45
CC
CC RESULT 15;
CC ID CARB_AQUAE STANCAP; PRC; 542 AA;
CC AC 567213;
CC DT 24-FEB-2003 (Pct. 41; Created)
CC DI 24-FEB-2003 (Pct. 41; Last sequence update)
CC DE Carboxyl-terminal synthetase chain C-terminal section
CC EN (E.F.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
CC GN CAPH2_GA.A.1172
CC GE CAPH2_GA.A.1172
CC GS Aquifex aeolicus
CC HA Aquifex aeolicus
CC HC Aquifex aeolicus
CC ID NCBI_TaxID=53361;
CC CX NCBI_TaxID=53361;
CC
CC SEQUENCE FROM N.A.
CC SPAINCAP; 513 aa; EMBL=567720;
CC Secrist J.E., Warren J.V., Gaasterland T., Young W.G., Locock A.L.,
CC Szlan D.E., Overbeek K., Snead M.A., Keller M., Aubley M., Huber R.,
CC Feldman R.A., Short J.M., Olson G.J., Sanson R.V.;
CC "The complete genome of the hyperthermophilic bacterium Aquifex
CC aeolicus".
CC EC Nature 392:333-338(1998);
CC CC -- CATALYTIC ACTIVITY: 2 ATP + L-glutamate + CO(2) -> H(2O) - 2 ADP +
CC -- Phosphate + L-gluccinate + carbamoyl phosphate [By similarity].
CC CC -- PATHWAY: Arginine biosynthesis per subunit [By similarity];
CC CC -- PATHWAY: Pyrimidine biosynthesis; first step.
CC CC -- SUBUNIT: Composed of two chains; the small (or q-utamine) chain
CC CC promotes the hydrolysis of glutamine to ammonia, which is used by
CC CC the large (or ammonia) chain to synthesize carbamoyl phosphate (by
CC CC similarity);
CC CC -- SIMILARITY: BELONGS TO THE CARB FAMILY. C-TERMINAL SECTION.
CC CC -- CATION: Sequence of CARB is split into two genes in A.aeolicus
CC CC (AC1172 and AC1193);
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announc/c
CC or send an email to licensel@isb-sib.ch);
CC
CC EXHL AEU07791; AEU07792;
CC DR EUB_ F1445; F14450;
CC RSSP; PG0765; BMK
CC HAMAP; MF_0210; AT09341; 1;

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DR  InterPro: IPRO05463; CPhase_L.
CR  InterPro: IPRO05479; CPhase_L-D2.
DR  InterPro: IPRO05481; CPhase_L-D2.
DR  InterPro: IPRO05482; CPhase_L-N.
DR  InterPro: IPRO004362; MGS-like.
DR  Pfam: PF03788; CPhase_L-chain.
DR  Pfam: PF03192; MGS85_L-D2.
DR  Pfam: PF03099; CPhase.
DR  PRINTS: PR03069; CPhase.
DR  PROSITE: PSJ0866; CPhase_L.
DR  PROSITE: PSJ0867; CPhase_L.
DR  PROSITE: PSJ0867; CPhase_L.
KW  Arginine biosynthesis; Pyrimidine biosynthesis; Lysase; ACP-Ligase;
KW  N-manganoate; Complete proteome.
FT  DOMAIN 1 357 CARBAVOYL PHOSPHATE SYNTHETIC DOMAIN.
FT  DOMAIN 398 537 ALLCETOYL DOMAIN.
FT  METAL 272 272 MANGANESE 3 (BY SIMILARITY).
FT  METAL 284 284 MANGANESE 3 (BY SIMILARITY).
FT  METAL 284 284 MANGANESE 3 (BY SIMILARITY).
SQ  SEQUENCE 537 AA; 60037 MW; 9C777FD2FD08D656 DCS4;
Query Match 82 %; Score 32; DB 1; length 537.
Best Local Similarity 100.0%; Pred. NO. 82;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps
QY 1 SILEY: 6
1 1 1
2b 299 SILEY: 304
Search completed: October 2, 2003, 13:55:19
Job time : 13 secs

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GenCode version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw mode:

Run on: October 2, 2003, 13:52:13
(without alignments)
56,445 Million cell updates/sec

Title: us-09-990-832c-51

Perfect score: 1 SIOPLP 7

Sequence: 1 SIOPLP 7

Scoring table: BLASTX2

Gapop 10.0 - Gapext 0.5

Searched: 840525 seqs, 25502604 residues

Total number of hits satisfying chosen parameters: 840525

Minimum DB seq length: 3

Maximum DB seq length: 2600000000

Post-processing: Minimum Match 0.8

Maximum Match 1.004

Clustering first 4% summaries

Database: SPCEMBL_21

1: sp-archaea

2: sp-bacteria

3: sp-fungi

4: sp-human

5: sp-invertebrate

6: sp-mammal

7: sp-microbial

8: sp-phage

9: sp-plant

10: sp-rodent

11: sp-virus

12: sp-vertebrate

13: sp-unclassified

14: sp-unclassified

15: sp-bacteriophage

16: sp-bacteriophage

17: sp-archaeal

Fred No. is the number of results predicted by chance to have a score greater than the observed score. Fred No. is the number of results predicted by chance to have a score greater than the observed score, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	IR	ID	Description
1	37	54.9	602	16	Q9J2F1
2	36	52.3	286	16	Q9J2F1
3	35	52.3	212	16	Q9J2F1
4	34	52.3	212	16	Q9J2F1
5	33	52.3	212	16	Q9J2F1
6	33	52.3	212	16	Q9J2F1
7	33	52.3	212	16	Q9J2F1
8	33	52.3	212	16	Q9J2F1
9	33	52.3	212	16	Q9J2F1
10	33	52.3	212	16	Q9J2F1
11	33	52.3	212	16	Q9J2F1
12	33	52.3	212	16	Q9J2F1
13	33	52.3	212	16	Q9J2F1
14	33	52.3	212	16	Q9J2F1
15	33	52.3	212	16	Q9J2F1

17	45	89.7	1791	5	Q9J2F1
18	44	87.2	205	10	Q9J2F1
19	44	87.2	218	2	Q9J2F1
20	44	87.2	218	2	Q9J2F1
21	44	87.2	218	2	Q9J2F1
22	44	87.2	218	2	Q9J2F1
23	44	87.2	218	2	Q9J2F1
24	44	87.2	218	2	Q9J2F1
25	44	87.2	218	2	Q9J2F1
26	44	87.2	218	2	Q9J2F1
27	44	87.2	218	2	Q9J2F1
28	44	87.2	218	2	Q9J2F1
29	44	87.2	218	2	Q9J2F1
30	44	87.2	218	2	Q9J2F1
31	44	87.2	218	2	Q9J2F1
32	44	87.2	218	2	Q9J2F1
33	44	87.2	218	2	Q9J2F1
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35	44	87.2	218	2	Q9J2F1
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37	44	87.2	218	2	Q9J2F1
38	44	87.2	218	2	Q9J2F1
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40	44	87.2	218	2	Q9J2F1
41	44	87.2	218	2	Q9J2F1
42	44	87.2	218	2	Q9J2F1
43	44	87.2	218	2	Q9J2F1
44	44	87.2	218	2	Q9J2F1
45	44	87.2	218	2	Q9J2F1

ADJUSTMENTS

17	45	89.7	1791	5	Q9J2F1
18	44	87.2	205	10	Q9J2F1
19	44	87.2	218	2	Q9J2F1
20	44	87.2	218	2	Q9J2F1
21	44	87.2	218	2	Q9J2F1
22	44	87.2	218	2	Q9J2F1
23	44	87.2	218	2	Q9J2F1
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27	44	87.2	218	2	Q9J2F1
28	44	87.2	218	2	Q9J2F1
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31	44	87.2	218	2	Q9J2F1
32	44	87.2	218	2	Q9J2F1
33	44	87.2	218	2	Q9J2F1
34	44	87.2	218	2	Q9J2F1
35	44	87.2	218	2	Q9J2F1
36	44	87.2	218	2	Q9J2F1
37	44	87.2	218	2	Q9J2F1
38	44	87.2	218	2	Q9J2F1
39	44	87.2	218	2	Q9J2F1
40	44	87.2	218	2	Q9J2F1
41	44	87.2	218	2	Q9J2F1
42	44	87.2	218	2	Q9J2F1
43	44	87.2	218	2	Q9J2F1
44	44	87.2	218	2	Q9J2F1
45	44	87.2	218	2	Q9J2F1

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

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Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum

Q9J2F1: Chlamydia muridarum


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DO 155 INFF.P 160

RESULT 7
QBQ62 PRELIMINARY: FRT: 287 AA.
AC QBQ62
CT 01-MAR-2003 (FIREMIRL 23, Created)
CT 01-MAR-2003 (FIREMIRL 23, Last sequence update)
CT 01-MAR-2003 (FIREMIRL 23, Last annotation update)
DE Kof-like protein. EN27.
DS Streptomyces sp. EN27.
EC 3.4.21.18.
CC Actinobacteria; Actinobacteriales; Streptomyces.
CX NCBI_TaxID:211464.
PR 1.
PF SEQUENCE FROM N.A.
PC STRAIN:EN27.
PA Combes J.T., Franco C.M.P., Ioria R.,
RI "Complete sequencing and analysis of pBN703, a novel 11kb plasmid
RI for an endospore-forming Streptomyces sp."
RI Published online 2002.
DE ENML AF513-81; AA#5284.1.
KW F.amid
SQ SEQUENCE 287 AA; 31911 MG; C78202F247A464 CRC64;
Query Match: 89.7%; Score 15. DP 2; Length 287.
Best Local Similarity 71.44; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0.
CY 1 SUFFP 7
DO 249 ACCEP.P 245

RESULT 8
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AC QBQ62
CT 01-MAR-2002 (FIREMIRL 23, Created)
CT 01-MAR-2002 (FIREMIRL 23, Last sequence update)
CT 01-MAR-2002 (FIREMIRL 23, Last annotation update)
DE ACV-CGA synthetases (AMP-forming/AMP-acid ligases I).
DS ACV-CGA synthetases.
EC 6.3.1.13.
CC Thermoterrificum thermophilus.
CX NCBI_TaxID:15970.
PR 1.
PF SEQUENCE FROM N.A.
PC STRAIN:M4507.
PA Chen Y., Xiao Y., Li X., Guo Z., Xu Z., Hu S., Tang X., Yang J.,
PA Qian Y., Xue Y., Li X., Guo X., Huang L., Dong X., Ma Y., Ling L.,
PA Cai H., Chen K., Ma J., Guo J., Yu J., Yang H.
CT *A complete sequence of T. thermophilus genome.*
DS Genome Res. 12:649-709(2002).
EC 6.3.1.13.
CX NCBI_TaxID:15970.
PR 1.
PF SEQUENCE FROM N.A.
PC STRAIN:M4507.
PA Chen Y., Xiao Y., Li X., Guo Z., Xu Z., Hu S., Tang X., Yang J.,
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